

15. (Amended) The method of claim 1, wherein the population prior genotype probability for the individual and said each candidate population is uniform.

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16. (Amended) The method of claim 1, wherein marker locus genotypes for said each candidate population are in Hardy-Weinberg Equilibrium and Gametic Phase Equilibrium.

17. (Amended) The method of claim 1, wherein marker locus genotypes for said each candidate population are not in Hardy-Weinberg Equilibrium or Gametic Phase Equilibrium.

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20. (Amended) The method of claim 1, wherein the alleles at the one or more marker loci are selected based on additive effects of the alleles on a desirable trait such that said assigning is based on the desirable trait.

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22. (Amended) The method of claim 1, wherein the alleles at the one or more marker loci are selected based on additive effects of the alleles on an undesirable trait such that said assigning is based on the undesirable trait.

REMARKS

Claims 1-3, 5-6, 8-9, 11-12, 14-17, 20, and 22 have been amended. Claims 1-23 are currently pending in the case. Further examination and reconsideration of the presently claimed application is respectfully requested.

Section 112, 2nd Paragraph, Rejections:

Claims 1-23 were rejected under 35 U.S.C. § 112, second paragraph, as being indefinite for failing to particularly point out and distinctly claim the subject matter which applicant regards as the invention. Claims 1-3, 5-6, 8-9, 11-12, 14-17, 20, and 22 have been amended for clarification and to correct antecedent problems in these claims.

The Office Action lists several claims that were rejected as containing recitations that are contended to be unclear or not defined in the specification. The Office Action also contends that some

claims are indefinite over a particular recitation because it is not clear how the recitation is determined. The recitations under contention include “a population prior genotype probability,” “knowledge concerning the individual which is available prior to genotyping the individual,” “population genotype probability,” how a “null hypothesis” relates to other elements of claim 1, “population posterior probability,” “a most likely population of origin,” “a threshold value,” “desirable trait,” and “undesirable trait.” The § 112, second paragraph, rejections of the claims as containing unclear or indefinite recitations are respectfully traversed.

The above recitations define in the claims what the Applicants regard as their invention in terms that they have chosen. In addition, the chosen terms are not used in ways that are contrary to accepted meanings in the art. A fundamental principle contained in 35 U.S.C. 112, second paragraph is that applicants are their own lexicographers. They can define in the claims what they regard as their invention essentially in whatever terms they choose so long as the terms are not used in ways that are contrary to accepted meanings in the art. MPEP 2173.01. Therefore, the above recitations are not indefinite.

In addition, if the claims containing the above recitations are analyzed in light of the contents of the particular application disclosure, the claims are definite. For example, if the recitations “a population prior genotype probability” and “knowledge concerning the individual which is available prior to genotyping the individual” are analyzed in light of the contents of the application disclosure on page 18, line 10 - page 19, line 14, for example, then it is clear that the claims containing these recitations set out and circumscribe the subject matter with a reasonable degree of clarity and particularity. The essential inquiry pertaining to this requirement is whether the claims set out and circumscribe a particular subject matter with a reasonable degree of clarity and particularity. Definiteness of claims language must be analyzed, not in a vacuum, but in light of: (A) The content of the particular application disclosure; (B) The teachings of the prior art; and (C) The claim interpretation that would be given by one possessing the ordinary level of skill in the pertinent art at the time the invention was made. MPEP 2173.02. In a similar manner, if the recitation “population genotype probability” and how the recitation “null hypothesis” relates to other elements of claim 1 are analyzed in light of the contents of the application disclosure on page 19, line 16 - page 21, line 15, for example, then it is clear that the claims containing these recitations also set out and circumscribe the subject matter with a reasonable degree of clarity and particularity. In addition, if the recitation “population posterior probability” is analyzed in light of the contents of the application disclosure on page 21, lines 17-19, for example, then it is clear that the claims containing this recitation also set out and circumscribe the subject matter with a reasonable degree of clarity and particularity.

Furthermore, if the recitation “a most likely population of origin” is analyzed in light of the contents of the application disclosure on page 21, lines 18-22, for example, then it is clear that the claims containing these recitations also set out and circumscribe the subject matter with a reasonable degree of clarity and particularity. If the recitations “a threshold value,” “desirable trait,” and “undesirable trait” are analyzed in light of the contents of the application disclosure, for example, on page 22, lines 14-29, on page 12, line 27 - page 14, line 6, and on page 14, lines 8-11, respectively, then it is clear that the claims containing these recitations set out and circumscribe the subject matter with a reasonable degree of clarity and particularity. Furthermore, if the above claim language is analyzed in light of the claim interpretation that would be given to the claims by one possessing the ordinary level of skill in the pertinent art at the time the invention was made, then the claim language is definite.

Although “most likely” is a term of degree, it does not render the claims indefinite. The fact that claim language, including terms of degree, may not be precise, does not automatically render the claim indefinite under 35 U.S.C. 112, second paragraph. *Seattle Box Co., v. Industrial Crating & Packing, Inc.*, 731 F.2d 818, 221 USPQ 568 (Fed. Cir. 1984). When a term of degree is presented in a claim, first a determination is to be made as to whether the specification provides some standard for measuring that degree. MPEP 2173.05(b). The Specification, for example, on page 21, lines 18-22, provides a standard for determining the “most likely” population of origin. Furthermore, the claim itself provides a standard for measuring a “most likely” population of origin. For example, claim 1 recites, in part: “the most likely population of origin has the largest population posterior genotype probability among the set of candidate populations.” Therefore, this claim language is acceptable because one of ordinary skill in the art would understand what is claimed, in light of the claims and the specification. Acceptability of the claim language depends on whether one of ordinary skill in the art would understand what is claimed in light of the specification. MPEP 2173.05(b).

Furthermore, it appears that the claims containing the above recitations were rejected solely because of the type of language chosen to define the subject matter for which patent prosecution is sought. As noted by the court in *In re Swinehart*, 439 F.2d 210, 160 USPQ 226 (CCPA 1971), a claim may not be rejected solely because of the type of language used to define the subject matter for which patent protection is sought. MPEP 2173.01. Some latitude in the manner of expression and the aptness of terms should be permitted even though the claim language is not as precise as the examiner might desire. MPEP 2173.02.

For at least the aforementioned reasons, claims 1-23 are definite. Accordingly, removal of the § 112 rejections of claims 1-23 is respectfully requested.

Examiners are encouraged to suggest claim language to applicants to improve the clarity or precision of the language used, but should not reject claims or insist on their own preferences if other modes of expression selected by applicants satisfy the statutory requirement. MPEP 2173.02. Therefore, although the modes of expression selected by the Applicants are believed to satisfy the statutory requirements under § 112, second paragraph, if the § 112, second paragraph, rejections of the claims are maintained, Applicants respectfully request the Examiner to suggest claim language that would improve the clarity or precision of the language used.

Section 102 Rejections:

Claims 1-9, 14-16, and 18-19 were rejected under 35 U.S.C. § 102(b) as being anticipated by Waser et al. (Trends in Ecol. Evol. (1998) 13(2): 43-44; hereinafter “Waser”). As will be set forth in more detail below, the § 102 rejections of claims 1-9, 14-16, and 18-19 are respectfully traversed.

The standard for “anticipation” is one of fairly strict identity. A claim is anticipated only if each and every element as set forth in the claim is found, either expressly or inherently described, in a single prior art reference. *Verdegaal Bros. V. Union Oil Co. of California*, 814 F.2d 628, 631, 2 USPQ2d 1051, 1053 (Fed. Cir. 1987), MPEP § 2131. The cited art does not disclose all limitations of the currently pending claims, some distinctive limitations of which are set forth in more detail below.

The cited art does not disclose determining a population prior genotype probability for an individual and each candidate population using knowledge concerning the individual which is available prior to genotyping the individual. Amended independent claim 1 recites in part: “determining a population prior genotype probability for an individual and said each candidate population using knowledge concerning the individual which is available prior to genotyping the individual.”

Waser discloses using an “assignment test” and a “shared allele” index to demonstrate that the Skjern River salmon population are descendants of old Danish stock. Waser, however, does not disclose determining a population prior genotype probability for an individual and each candidate population using knowledge concerning the individual which is available prior to genotyping the individual. For example,

Waser states that “one types the trophy at multiple loci and calculates the expected frequency of the trophy’s genotype in each putative source population. The genotype is assigned to the population where its expected frequency is highest, that is, where it has the greatest probability of occurrence.” (Waser -- page 43, col. 2.) Therefore, Waser discloses one example of the assignment test that does not include determining a population prior genotype probability for the trophy. Waser also discloses that assigning a genotype to a population includes steps (1) - (5) listed in Box 1 on page 43 of Waser. However, none of these steps includes determining a population prior genotype probability for an individual. In addition, Waser states that step (1) of the assignment test includes removing “the test individual’s genotype from the population it was sampled in.” (Waser -- page 43, Box 1). Therefore, although Waser discloses that an individual is part of a sampled population prior to other steps in the assignment test, Waser does not disclose determining a population prior genotype probability that the individual belongs to any one population. As such, Waser does not teach or suggest determining a population prior genotype probability for an individual and each candidate population using knowledge concerning the individual which is available prior to genotyping the individual, as recited in claim 1. Consequently, Waser does not teach or suggest all limitations of claim 1.

The cited art does not disclose sequentially determining a population genotype probability for an individual and each candidate population based on a genotype of the individual under a null hypothesis that the individual arose from each candidate population. Amended independent claim 1 recites in part: “sequentially determining a population genotype probability for the individual and said each candidate population based on the genotype of the individual under a null hypothesis that the individual arose from said each candidate population.”

Waser, however, does not disclose sequentially determining a population genotype probability for an individual and each candidate population based on a genotype of the individual under a null hypothesis that the individual arose from each candidate population. For example, Waser states that step (1) of the assignment test includes removing “the test individual’s genotype from the population it was sampled in and estimate allele frequencies at each locus.” (Waser -- page 43, Box 1). Waser states that step (2) of the assignment test includes determining “the genotype’s expected frequency in that population at each locus.” (Waser -- page 43, Box 1). In addition, Waser discloses that step (3) of the assignment test includes multiplying across loci and log-transforming the product. Waser also discloses that the assignment test includes assigning “the genotype to the population in which it has the highest log likelihood of occurrence.” (Waser -- page 43, Box 1). Therefore, none of the steps in Waser’s assignment test includes

using a null hypothesis that the individual arose from each candidate population. For example, in contrast to the teachings of Waser, the Specification states “under the null hypothesis that the individual originated from the i^{th} population, the individual may be incorporated into the sample data for this population and the allele counts at each locus updated.” (Specification -- page 19, line 31 - page 20, line 3). It is known in the art that under the null hypothesis, which begins with the assumption that the null hypothesis is true, or as applied to the presently claimed invention, that an individual does belong to a population, incorporating test data for the individual into sample data for the population and updating the sample data of the population is theoretically correct. As shown above, however, the teachings of Waser do not include incorporating the individual into the sample data for a population and updating the allele counts at each locus. As such, Waser cannot teach or suggest sequentially determining a population genotype probability for an individual and each candidate population based on a genotype of the individual under a null hypothesis that the individual arose from each candidate population, as recited in claim 1. Consequently, Waser does not teach or suggest all limitations of claim 1.

The cited art does not disclose combining a population prior genotype probability and a population genotype probability to obtain a population posterior genotype probability for the individual and each candidate population. Amended independent claim 1 recites in part: “combining the population prior genotype probability from step (b) and the population genotype probability from step (d) to obtain a population posterior genotype probability for the individual and each candidate population.”

For at least the aforementioned reasons, Waser does not teach or suggest determining a population prior genotype probability, as recited in step (b) of claim 1, or determining a population genotype probability, as recited in step (d) of claim 1. As such, Waser cannot teach or suggest combining a population prior genotype probability and a population genotype probability to obtain a population posterior genotype probability for the individual and each candidate population, as recited in claim 1. Consequently, Waser does not teach or suggest all limitations of claim 1.

The cited art does not disclose computing an additional probability with which genotypes rarer than the individual’s genotype occur in the most likely population of origin. Amended claim 3 recites in part: “computing an additional probability with which genotypes rarer than the individual’s genotype occur in the most likely population of origin.”

Waser does not disclose computing an additional probability with which genotypes rarer than the individual's genotype occur in the most likely population of origin. For example, Waser states:

a problem arises when the test genotype contains an apparently unique allele. Because this situation might arise from sampling error, the unique allele is added to all test populations at a small frequency, e.g. $1/2N$ copies. This convention differs slightly from that originally proposed and assigns individuals with less bias when populations differ in size. In this form, the assignment test is essentially the 'leave one out' technique of crossvalidation in discriminant analysis. (Waser -- page 43, Box 1).

Therefore, although Waser discloses a method for addressing the problem that arises when a test genotype contains an apparently unique allele, the method of Waser includes steps to determine if the allele appears unique due to sampling error. However, Waser does not teach or suggest computing an additional probability with which genotypes rarer than the individual's genotype occur in the most likely population of origin, as recited in claim 3. Consequently, Waser does not teach or suggest all limitations of claim 3.

For at least the aforementioned reasons, claim 1, as well as claims dependent therefrom, are not anticipated by the cited art. Accordingly, removal of the § 102 rejections of claims 1-9, 14-16, and 18-19 is respectfully requested.

Section 103 Rejections:

Claims 10-13 and 17 were rejected under 35 U.S.C. § 103(a) as being unpatentable over Waser in view of U.S. Patent No. 6,183,955 to Andersson et al. (hereinafter "Andersson"). Claims 20-21 were rejected under 35 U.S.C. § 103(a) as being unpatentable over Waser in view of Stone et al. (J. Anim. Sci. (June 1999) Vol. 77 (6): 1379-1384; hereinafter "Stone"). Claims 22-23 were rejected under 35 U.S.C. § 103(a) as being unpatentable over Waser in view of Keele et al. (J. Anim. Sci. (June 1999) Vol. 77 (6): 1364-1371; hereafter "Keele"). As set forth in more detail below, the § 103 rejections of claims 10-13, 17, and 20-23 are respectfully traversed.

To establish a *prima facie* obviousness of a claimed invention, all claim limitations must be taught or suggested by the prior art. *In re Royka*, 490 F.2d 981, 180 U.S.P.Q. 580 (C.C.P.A. 1974), MPEP 2143.03. Obviousness cannot be established by combining or modifying the teachings of the prior art to produce the claimed invention, absent some teaching or suggestion or incentive to do so. *In re Bond*, 910 F. 2d 81, 834, 15 USPQ2d 1566, 1568 (Fed. Cir. 1990). The cited art does not teach, suggest, or provide

motivation for all limitations of the currently pending claims, some distinctive limitations of which are set further in more detail below.

None of the cited art teaches or suggests the claimed determining a population prior genotype probability, the claimed sequentially determining a population genotype probability, or the claimed combining a population prior genotype probability and a population genotype probability to obtain a population posterior genotype probability for the individual and each candidate population, as recited in claim 1. As set forth in more detail above, Waser does not teach or suggest these limitations of claim 1. For at least the aforementioned reasons, Waser also does not provide motivation for these limitations of claim 1.

Andersson discloses a method for determining the coat color genotype of a pig. Stone discloses a primary screen of the bovine genome for quantitative trait loci affecting carcass and growth traits. Keele discloses a region on bovine chromosome 15 that influences beef longissimus tenderness in steers. Neither Andersson, Stone, nor Keele, however, disclose the claimed determining a population prior genotype probability, the claimed sequentially determining a population genotype probability, or the claimed combining a population prior genotype probability and a population genotype probability to obtain a population posterior genotype probability for the individual and each candidate population. As such, Waser, Andersson, Stone, and Keele, either individually or in any combination, do not teach, suggest, or provide motivation for the claimed determining a population prior genotype probability, the claimed sequentially determining a population genotype probability, or the claimed combining a population prior genotype probability and a population genotype probability to obtain a population posterior genotype probability for the individual and each candidate population, as recited in claim 1. Consequently, Waser, Andersson, Stone, and Keele, either individually or in combination, do not teach or suggest all limitations of claim 1.

Furthermore, the limitations of the presently claimed invention that are not taught or suggested by the cited art, either individually or in combination, provide several advantages over the cited art. For example, as set forth in the Specification, “the approach assumes that any allele that is present in an individual to be tested but that is absent from the sample for any one candidate population, is absent because it is a rare allele that was not capture in the sample rather than the allele being population specific.” (Specification -- page 25, lines 16-21). In addition, the Specification states that “on the other hand, our approach gains specificity in that populations are not rejected from consideration simply because

an allele was not present in the sample of individuals drawn from the population.” (Specification -- page 25, line 33, page 26, line 4). This advantage is realized in the presently claimed invention, at least in part, because the claimed sequentially determining a population genotype probability is performed using a null hypothesis. For example, using the null hypothesis avoids problems of estimability (i.e., a discontinuity) that may be caused when the individual possesses an allele that was not detected in the original sample that was drawn from the population. Therefore, the presently claimed invention provides several advantages over the cited art.

None of the cited art discloses computing an additional probability with which genotypes rarer than the individual’s genotype occur in the most likely population of origin, as recited in claim 3. As set forth in more detail above, Waser does not teach or suggest these limitations of claim 3. For at least the aforementioned reasons, Waser also does not provide motivation for these limitations of claim 3. In addition, neither Andersson, Stone, nor Keele disclose computing an additional probability with which genotypes rarer than the individual’s genotype occur in the most likely population of origin. As such, Waser, Andersson, Stone, and Keele, either individually or in any combination, do not teach, suggest, or provide motivation for computing an additional probability with which genotypes rarer than the individual’s genotype occur in the most likely population of origin, as recited in claim 3. Consequently, Waser, Andersson, Stone, and Keele, either individually or in combination, do not teach or suggest all limitations of claim 3.

The cited art does not disclose determining a population prior genotype that is based on one or more morphological features of the individual. Claim 10 recites in part: “the population prior genotype probability is based on one or more morphological features of the individual.”

The Office Action states: “Waser does not teach assigning an individual by genotyping based on a morphological feature, such as coat color.” (Office Action -- page 5). The Office Action also states that “in view of the teachings of Andersson, it would have been obvious to one of ordinary skill in the art at the time the invention was made to have modified the method of Waser so as to have assigned a pig to a population based on color coat.” (Office Action -- page 6). However, Andersson states:

the gene determining whether the animal is coloured or the desired white is designated I (for inhibition of coat colour). The version of the gene preventing the expression of any colour (I) is dominant to that which allows colour to develop (i). Traditional selection for white animals has

reduced the frequency of i, but it still remains in the population in white heterozygous carrier animals. These animals can only be identified when they produce coloured offspring through matings with other heterozygous animals. (Andersson -- col. 1, lines 44-52).

Therefore, Andersson teaches that although animals may be in the same population, they may have a different coat color. In this manner, Andersson cannot teach or suggest assigning a pig to a population based on coat color as contended in the Office Action. In addition, Andersson, Stone, and Keele do not teach or suggest determining a population prior genotype that is based on one or more morphological features of the individual, as recited in claim 10. As such, Waser cannot be modified by any of the cited art to remedy the deficiencies therein. Consequently, none of the cited art, either individually or in combination, teaches, suggests, or provides motivation for all limitations of claim 10.

For at least the reasons stated above, none of the cited art teaches or suggests the limitations of claim 1. Therefore, claim 1, and claims dependent therefrom, are patentably distinct over the cited art. Accordingly, removal of the § 103(a) rejections of claims 10-13, 17, and 20-23 is respectfully requested.

NOTICE OF CHANGE OF ADDRESS

Applicant respectfully requests the Commissioner to change the correspondence address to the following:

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NOTICE OF CHANGE OF ATTORNEY DOCKET NUMBER

The Commissioner is requested to change the attorney docket number for the above-identified patent application as set forth below.

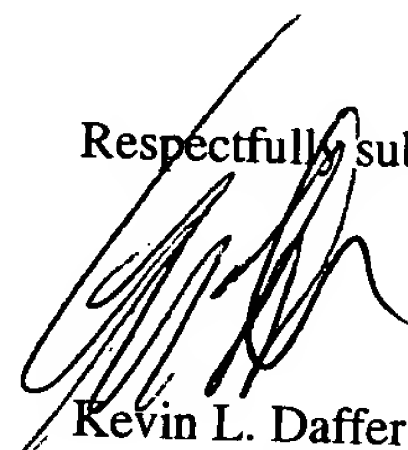
Old Number:	0987/62100/JRW/ADM
New Number:	5750-00200

CONCLUSION

In this response, claims 1-3, 5-6, 8-9, 11-12, 14-17, 20, and 22 have been amended. Rejections of claims 1-23 have been addressed. Therefore, this response constitutes a complete response to all of the issues raised in the Office Action mailed June 19, 2002. In view of the remarks traversing the rejections, Applicants assert that pending claims 1-23 are in condition for allowance. If the Examiner has any questions, comments, or suggestions, the undersigned earnestly requests a telephone conference.

The Commissioner is authorized to charge any required fees or credit any overpayment to Conley, Rose & Tayon, P.C. Deposit Account No. 50-1505/5750-00200.

Respectfully submitted,



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ATTACHMENT A
Pending Claims including "Marked-Up" Amendments

IN THE CLAIMS:

Please amend claims 1-3, 5-6, 8-9, 11-12, 14-17, 20, and 22 as follows:

1. (Amended) A method of assigning an individual to a population of origin, which comprises:
 - (a) identifying a set of candidate populations of origin, wherein each candidate population is characterized by genotype frequencies and allele frequencies at one or more marker loci;
 - (b) determining a population prior genotype probability for [each] an individual and said each candidate population [of origin] using knowledge concerning the individual which is available prior to genotyping the individual;
 - (c) genotyping the individual to identify [the] alleles at the one or more [of the] marker loci [identified] in step (a) to thereby identify the individual's genotype;
 - (d) [based on the identified genotype of the individual,] sequentially determining a population genotype probability for the individual and said each candidate population [of origin] based on the genotype of the individual under a null hypothesis that the individual arose from [the] said each candidate population;
 - (e) combining the population prior genotype probability from step (b) and the population genotype probability from step (d) to obtain a population posterior genotype probability for the individual and said each candidate population [of origin];
 - (f) identifying a most likely population of origin, wherein the most likely population of origin has the largest population posterior genotype probability among the set of candidate populations; and
 - (g) assigning the individual to the most likely population of origin identified in step (f).

2. (Amended) The method of claim 1, wherein the individual is only assigned to the most likely population of origin if the population posterior genotype probability for the most likely population of origin exceeds a threshold value.
3. (Amended) The method of claim 1, which further comprises:
 - (a) computing [a] an additional probability with which genotypes rarer than the individual's genotype occur in the most likely population of origin; and
 - (b) if the additional probability in step (a) is above a threshold value, assigning the individual to [the population of origin previously identified as] the most likely population of origin, or if the additional probability in step (a) is not above [a] the threshold value, assigning the individual to a novel population that is not represented among the set of candidate populations of origin.
4. The method of claim 2, wherein the threshold value is determined empirically.
5. (Amended) The method of claim 4, wherein the threshold value is determined using population posterior genotype probabilities of a sample of individuals from said each candidate population who are independent of individuals used to characterize said each candidate population.
6. (Amended) The method of claim 4, wherein the threshold value is varied to determine the percentage of a sample of individuals who a) cannot be classified [to a population of origin], b) are correctly classified, and c) are incorrectly classified.
7. The method of claim 3, wherein the threshold value is determined empirically.
8. (Amended) The method of claim 7, wherein the threshold value is determined using population posterior genotype probabilities of a sample of individuals from said each candidate population who are independent of individuals used to characterize said each candidate population.

9. (Amended) The method of claim 7, wherein the threshold value is [varied] increased to reduce the percentage of a sample of individuals who are incorrectly classified to [a population] one of the candidate populations of origin.
10. The method of claim 1, wherein the population prior genotype probability is based on one or more morphological features of the individual.
11. (Amended) The method of claim 10, wherein the one or more morphological features allow the exclusion of one or more of the candidate populations of origin.
12. (Amended) The method of claim 11, wherein the one or more morphological features are selected from the group consisting of coat color, presence or absence of horns, presence or absence of a shoulder hump, and presence or absence of a long, downswept ear.
13. The method of claim 12, wherein the coat color is black or nonblack.
14. (Amended) The method of claim 1, wherein the population prior genotype probability for the individual and said each candidate population is set to equal a proportion of total population size [that comprises] in said each candidate population [of origin].
15. (Amended) The method of claim 1, wherein the population prior genotype probability for the individual and said each candidate population is [assumed to be] uniform [for each candidate population of origin].
16. (Amended) The method of claim 1, wherein marker locus genotypes for said each candidate population [of origin] are in Hardy-Weinberg Equilibrium and Gametic Phase Equilibrium.
17. (Amended) The method of claim 1, wherein marker locus genotypes for said each candidate population [of origin] are not in Hardy-Weinberg Equilibrium or Gametic Phase Equilibrium.
18. The method of claim 1, wherein the individual is an animal.

19. The method of claim 18, wherein the animal is a cow, a heifer, a steer, a bull, a bullock, a pig, a horse, a fish, a chicken, a duck, a lamb, a shrimp, an oyster, a mussel, or a shellfish.
20. (Amended) The method of claim 1, wherein the alleles at the one or more marker loci are selected based on additive effects of the alleles on a desirable trait such that said assigning [wherein the candidate population of origin] is [selected] based on [a] the desirable trait.
21. The method of claim 20, wherein the desirable trait is selected from the group consisting of one or more of animal growth, quality grade, yield grade, marbling, rib-eye muscle area, dressing percentage, meat tenderness, meat flavor, meat palatability, fatness, fat color, unsaturated fatty acid content of fat, reproductive efficiency, prolificacy, disease resistance, feed conversion efficiency, drought tolerance, and heat tolerance.
22. (Amended) The method of claim 1, wherein the alleles at the one or more marker loci are selected based on additive effects of the alleles on an undesirable trait such that said assigning [wherein the candidate population of origin] is [selected] based on [an] the undesirable trait.
23. The method of claim 22, wherein the undesirable trait is toughness of meat.